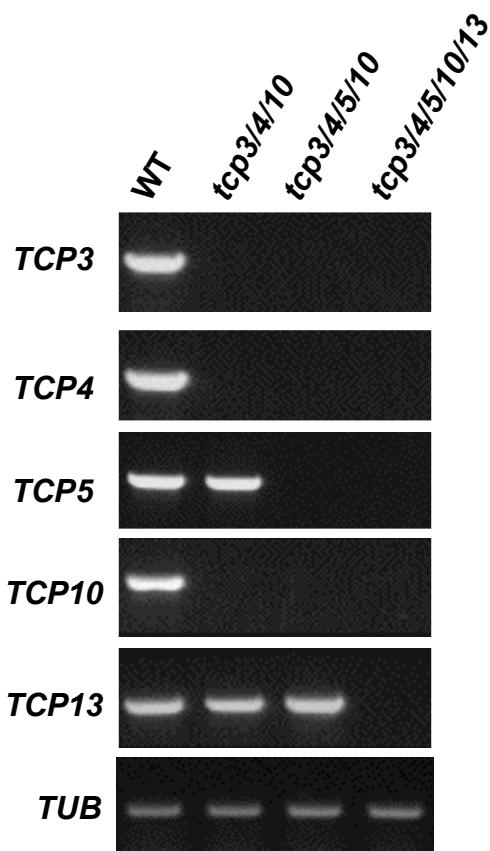
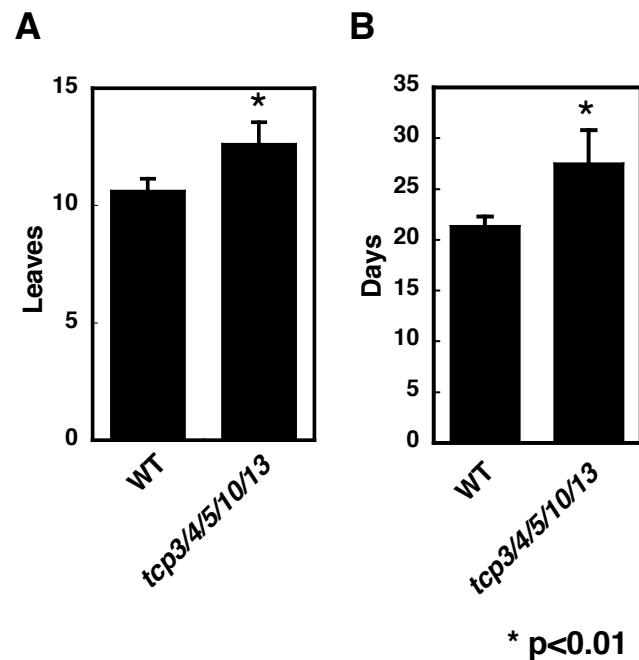


Supplemental Figure 1. Schematic diagram of the structures of C/N-like *TCP* genes and the sites of insertion of T-DNA into the respective genes.

White and grey boxes indicate coding regions and conserved TCP domains, respectively (<http://www.arabidopsis.org/>). Triangles indicate T-DNA insertion sites. Numbers show the positions of insertions relative to the sites of initiation of translation. We used *tcp4-1* to generate lines with multiple mutations.



Supplemental Figure 2. Expression of C/N-like *TCP* genes in *tcp* mutants. Total RNA was prepared from leaves and subjected to RT-PCR analyses.



Supplemental Figure 3. Delayed flowering of *tcp3/4/5/10/13* plants.

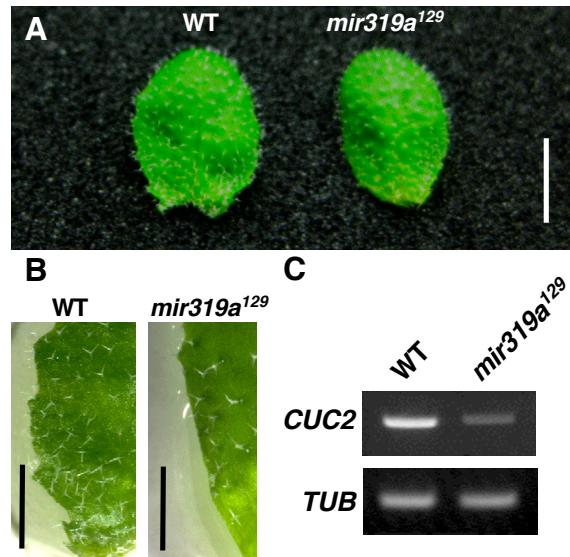
Flowering time was monitored in terms of the number of rosette leaves (**A**) and days after germination (**B**). Error bars indicate standard deviations (n=8) and asterisks indicate significant difference from the wild-type by Student's *t*-test (P < 0.01). Plants were grown under conditions of 16 h light/8 h dark.



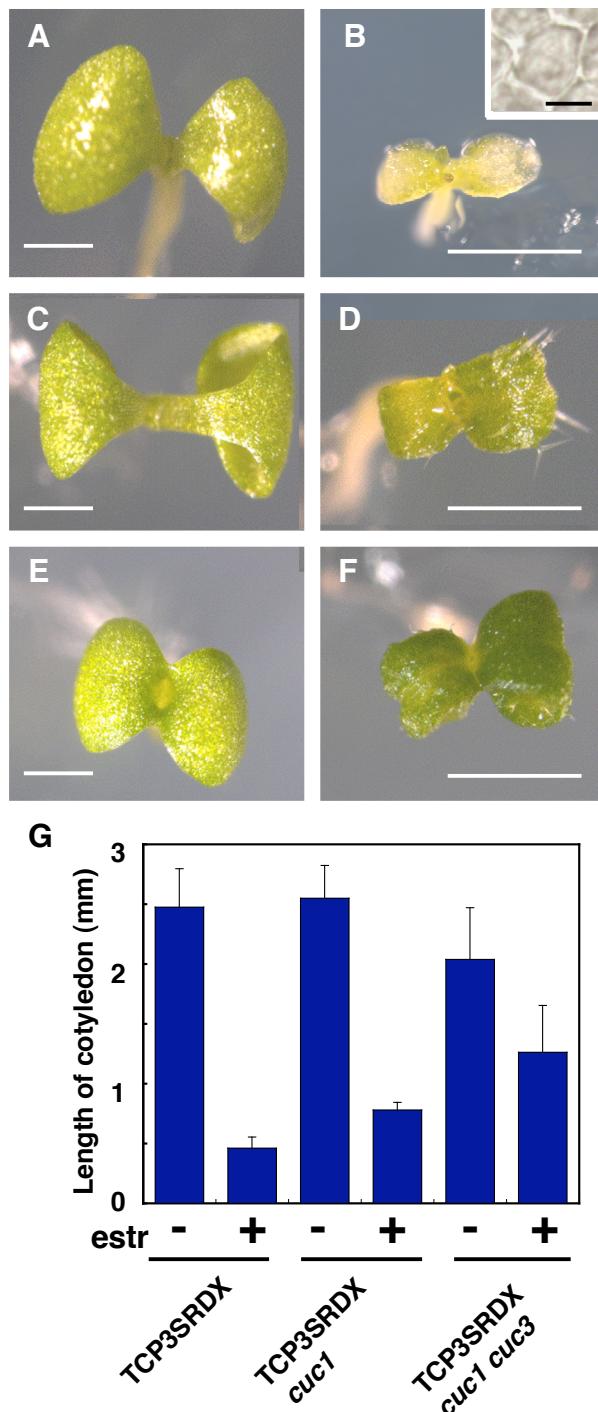
Supplemental Figure 4. Inflorescence stem of *Pro35S:miR319A tcp3/4/5/10/13*.

(A) The wild-type inflorescence at four weeks after germination.

(B) and (C) The *Pro35S:miR319A tcp3/4/5/10/13* inflorescences at five weeks after germination with elongating multiple stems, as indicated by asterisks (B), and with fasciated stems, as indicated by a triangle (C). The bolting of *Pro35S:miR319A tcp3/4/5/10/13* plants was delayed, probably due to knockout of multiple *TCP* genes (Supplemental Figure 3). Bars = 0.5 mm.



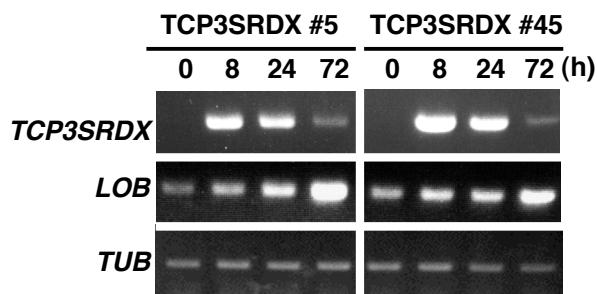
Supplemental Figure 5. Smooth margin of leaves and downregulation of *CUC2* in *mir319a¹²⁹*.
(A) Rosette leaves of wild-type (WT) and *mir319a¹²⁹* at the 17th position. *Lansberg erecta* (*Ler*) plants display mild serration of leaves and increased serration in successive leaves; therefore, the plants were grown for eight weeks under conditions of 10 h light/14 h dark.
(B) Close-up views of the margin of WT and *mir319a¹²⁹*. Bars = 5 mm in **(A)** and 1 mm in **(B)**.
(C) Expression of *CUC2* in leaves at the 16th to 19th positions from WT and *mir319a¹²⁹*. PCR was terminated after 36 cycles. Expression of tubulin (*TUB*) was monitored as an internal control.



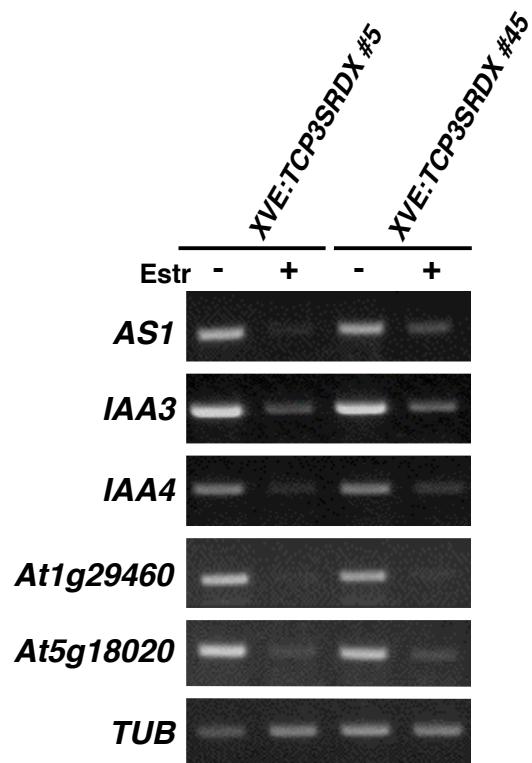
Supplemental Figure 6. Cotyledons of *ProXVE:TCP3SRDX*, *ProXVE:TCP3SRDX cuc1*, and *ProXVE:TCP3SRDX cuc1 cuc3* plants.

(A) through (F). Seedlings of *ProXVE:TCP3SRDX* (**A**) and (**B**), *ProXVE:TCP3SRDX cuc1* (**C**) and (**D**), and *ProXVE:TCP3SRDX cuc1 cuc3* (**E**) and (**F**) plants after exposure to DMSO (**A**), (**C**), and (**E**), and to 5 μ M estradiol (**B**), (**D**), and (**F**) for five days after germination on agar plates. The inset in (**B**) indicates the epidermal cells of *ProXVE:TCP3SRDX* with round shaped cotyledons after exposure to estradiol. *CUC* genes seemed not to be involved in the formation of trichomes on cotyledons (Figure 1A; Koyama et al. 2007). Bars = 1 mm in (**A**) through (**F**) and 10 μ m in the inset in (**B**).

(G) Lengths of cotyledons. Mutations in *CUC1* and *CUC3* allowed considerable recovery of the normal expansion of cotyledons that was limited by *TCP3SRDX*. Error bars indicate standard deviations (n=6 to 10).

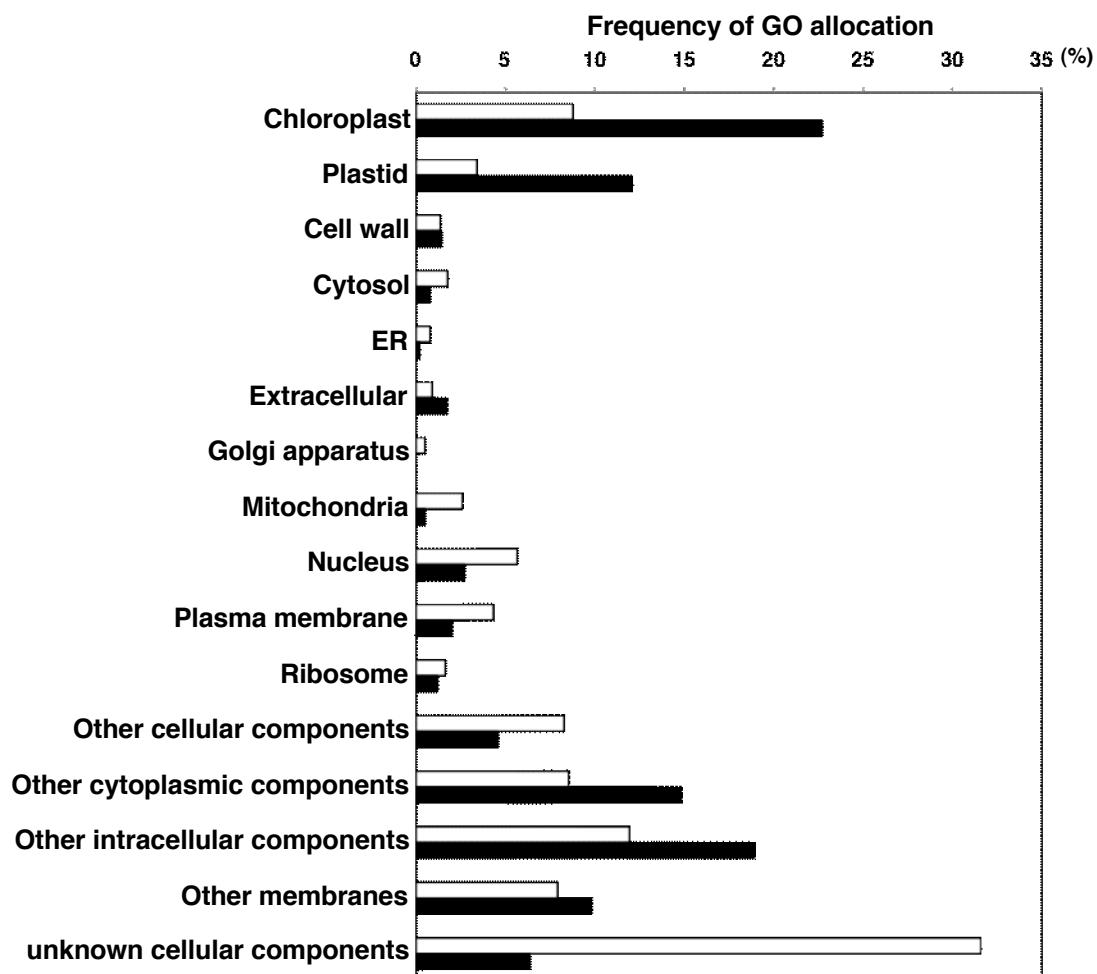


Supplemental Figure 7. Expression of *TCP3SRDX* and *LOB* after induction by estradiol. Two independent lines of *ProXVE:TCP3SRDX* plants, #5 and #45, were maintained in liquid medium and harvested at the times indicated after the start of exposure to estradiol. For detection of the expression of *TCP3SRDX*, PCR was terminated after 21 cycles. Expression of the *TUB* gene was monitored as an internal control.



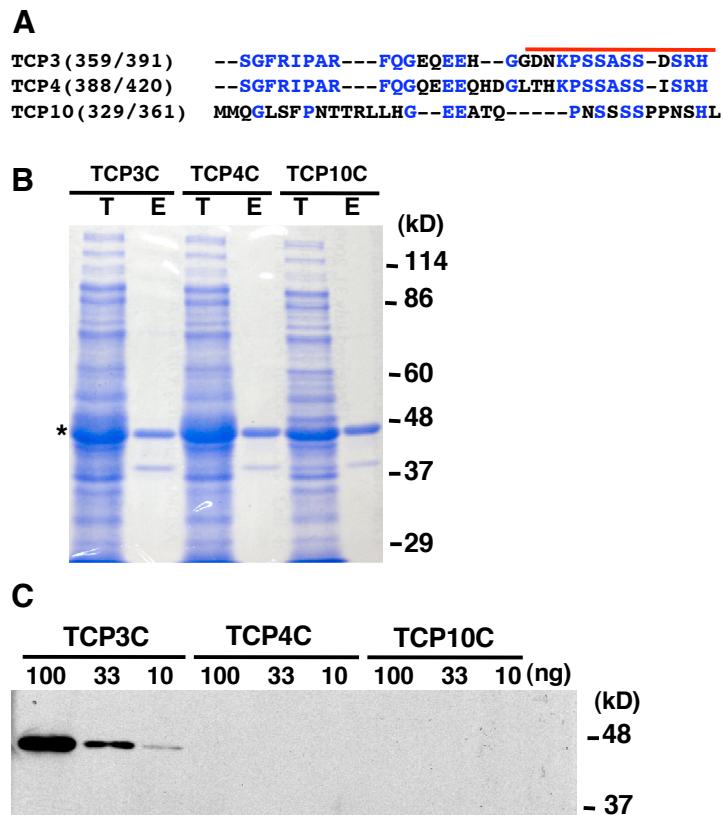
Supplemental Figure 8. Expression of the target genes of TCP3 at eight hours after induction of *TCP3SRDX*.

Two independent lines of *ProXVE:TCP3SRDX* plants, #5 and #45, were grown in liquid medium and harvested at eight hours after supplementation with DMSO (-) or 5 μ M estradiol (Estr; +). Expression of the *TUB* gene was monitored as an internal control.



Supplemental Figure 9. Functional categorization of genes downstream of TCP3 based on gene ontology (GO).

Each percentage was calculated from the number of genes allotted to the respective term per total number of genes in the genome (white bar) or downstream of TCP3 (black bar). The designations were derived from the GO cellular component at <http://www.arabidopsis.org/>. There were 30,994 genes in the genome and 1,107 genes downstream of TCP3.

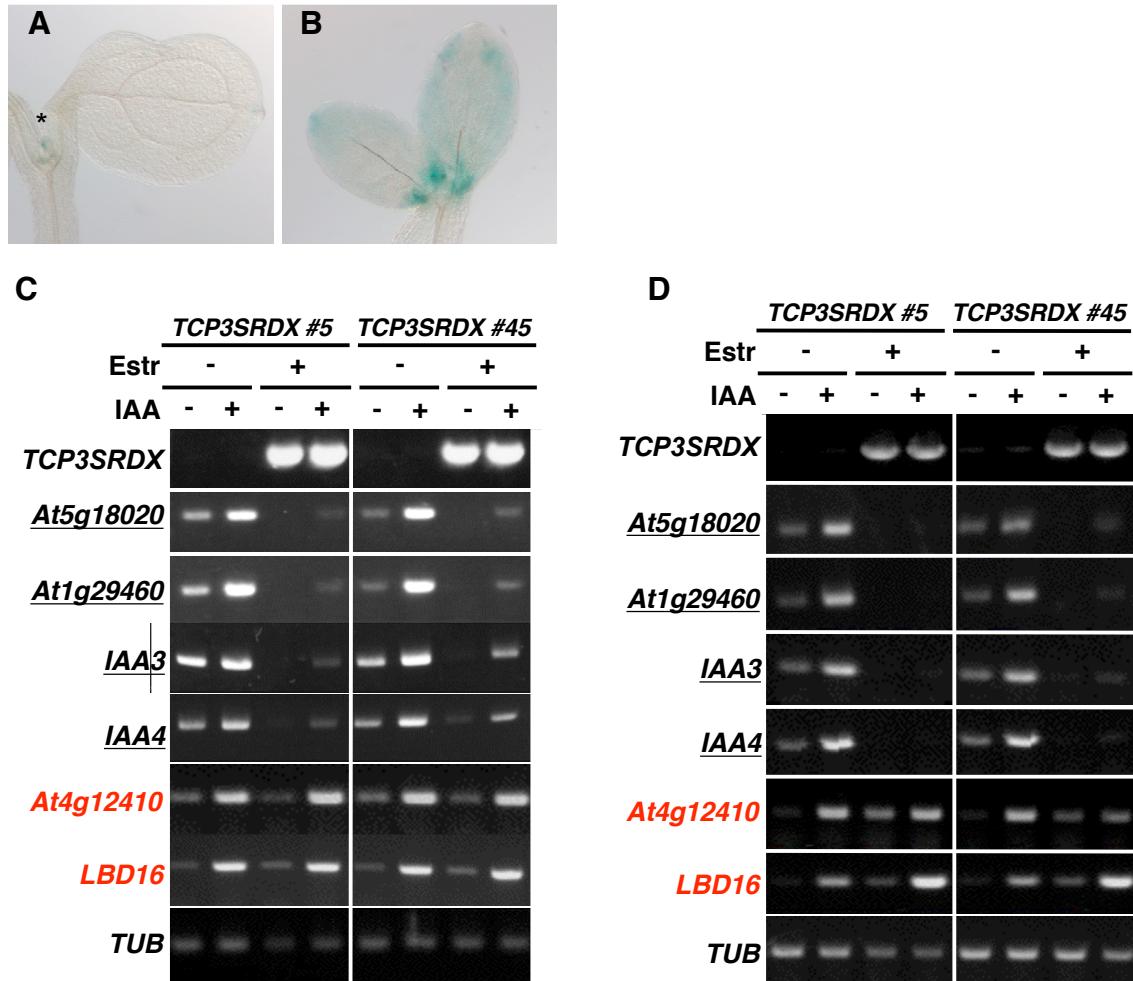


Supplemental Figure 10. Specificity of antibodies against TCP3 used in this study.

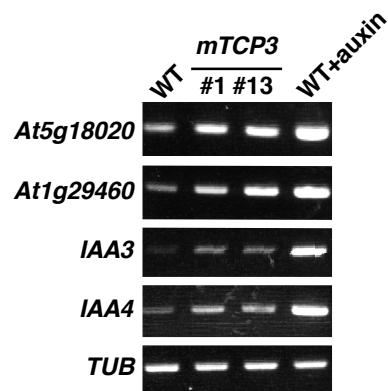
(A) An alignment of 33 amino acid residues in the carboxy terminus of TCP3, TCP4, and TCP10, showing the partial similarity among them. Blue letters indicate identical residues with those of TCP3. TCP3 has a highly conserved domain in the amino terminal and middle regions (Supplemental Figure 1); therefore, the carboxyl terminal residues (red bar) were used for the synthetic peptide.

(B) Expression and purification of the 33 residues of the carboxy terminus of TCP3, TCP4, and TCP10 (TCP3C, TCP4C, and TCP10C, respectively) fused with maltose-binding protein. The coding sequences for TCP3C, TCP4C, and TCP10C were individually cloned into *Eco* RI and *Sa* I sites of pMALc2 (New England Biolabs) and transformed to the *E. coli* BL21 cells. Bacterial proteins were purified using a batch method, as specified by the manufacturer. The total (T) and eluted (E) proteins were subjected to SDS-PAGE and visualized by Coomassie brilliant blue. Asterisks indicate the position of the bands corresponding to TCP3C, TCP4C, and TCP10C.

(C) Specificity of TCP3-specific antibodies in immunoblotting. The indicated amount of the purified protein for TCP3C, TCP4C, and TCP10C, respectively, were separated by SDS-PAGE and transferred to Immobilon-P (Millipore). The membrane was incubated with TCP3-specific antibodies at a dilution of 1:1,500 as the primary antibody and incubated with anti-rabbit IgG (GE Healthcare) at a dilution of 1:5,000 as the secondary antibody. Immunoreactive proteins were visualized using a Western Lightning Plus-ECL kit (PerkinElmer). The molecular size marker is shown at the right of the panels in **(B)** and **(C)**.



Supplemental Figure 11. Expression of auxin-inducible genes after continuous induction of *TCP3SRDX*. **(A)** and **(B)**. The activity of the *DR5* promoter after induction of *TCP3SRDX* for 24 h (**A**) and 48 h (**B**). *ProDR5:GUS ProXVE:TCP3SRDX* plants grown in liquid medium were subjected to the GUS assay after supplementation with 5 μ M estradiol for 24 h (**A**) and 48 h (**B**). An asterisk in (**A**) indicates the signal at the tip of expanding leaves. **(C)** and **(D)** Changes in expression of auxin-inducible genes by the induction of *TCP3SRDX* for 24 h (**C**) and 48 h (**D**). Total RNAs were prepared from two independent lines of *ProXVE:TCP3SRDX* plants grown in liquid medium with DMSO (-) or 5 μ M estradiol (Estr; +) for 23 h (**C**) and 47 h (**D**), before treatment with IAA for one hour. Black underlines and red letters indicate the direct target and non-direct target genes of TCP3, respectively. For detection of the expression of *TCP3SRDX*, PCR was terminated after 21 cycles. Expression of the *TUB* gene was monitored as an internal control.



Supplemental Figure 12. Expression of the target genes of TCP3 in *Pro35S:mTCP3* plants. Total RNAs were prepared from wild-type (WT) and two independent lines of *Pro35S:mTCP3* plants (*mTCP3*) grown on MS plates for seven days. The positive control sample was prepared from WT plants supplemented with 1 μ M NAA for one hour in liquid medium (WT + auxin). Expression of the *TUB* gene was monitored as an internal control.

Supplemental Table 1. Changes in expression of boundary-specific genes upon expression of *TCP3SRDX* determined by microarray analysis of *ProXVE:TCP3SRDX* plants.

AGI code	Name	^a change	^a P value	^a signal values (Estr/DMSO)		
At3g15170	CUC1	17.54	0.0001	0.712/0.038	0.912/0.052	0.792/0.047
At5g53950	^b CUC2	2.907	0.0129	0.196/0.087	0.254/0.079	0.237/0.072
At1g76420	CUC3	7.499	0.0009	0.482/0.071	0.532/0.063	0.520/0.070
At5g63090	LOB	2.438	0.0287	0.498/0.228	0.507/0.159	0.446/0.230
At1g55580	LAS	5.255	0.0795	0.023/0.003	0.025/0.013	0.031/0.003
At1g13710	^c CYP78A5/KLUH	3.773	0.0015	3.537/1.025	3.481/0.931	3.742/0.905
At3g57130	BOP1	4.002	0.0058	0.428/0.132	0.476/0.103	0.412/0.099

^aChanges are average ratios of triplicate signal values of *ProXVE:TCP3SRDX* plants exposed to DMSO relative to those from plants exposed to 5 μM estradiol (Estr) for 24 h in liquid medium. P values are obtained as described in Methods.

^b*CUC2* is also expressed in the serration of leaf margins (Nikovics et al. 2006).

^c*CYP78A5/KLUH* is also expressed at the tips of petals and sepals (Anastasiou et al. 2007).

References

- Nikovics, K., Blein, T., Peaucelle, A., Ishida, T., Morin, H., Aida, M., and Laufs, P. (2006). The balance between the *MIR164A* and *CUC2* genes controls leaf margin serration in *Arabidopsis*. *Plant Cell* 18, 2929-2945.
- Anastasiou, E., Kenz, S., Gerstung, M., MacLean, D., Timmer, J., Fleck, C., and Lenhard, M. (2007). Control of plant organ size by *KLUH/CYP78A5*-dependent intercellular signaling. *Dev. Cell* 13, 843-856.

Supplemental Table 2. Genes containing *cis* elements in their 1,000 bp upstream regions that are overrepresented in the genes downstream of TCP3

Rank ^a	Group of genes	Member ^b	Count ^c	P value ^d	Odds ratio ^e
1	GGnCCC motif ^f	5897	408	< 2.2e-16	1.84366
2	GTGGnCCC motif ^g	594	64	2.265e-10	2.605879
3	AtMYC2 binding site	9986	548	3.263e-08	1.39597
4	Ibox motif I	10974	587	3.723e-07	1.357627

^aFour *cis* elements with the lowest P values of the 113 *cis* elements examined.^bNumber of genes in the genome^cNumber of genes downstream of TCP3 that overlapped the group.^dValues from Fischer's exact test.^eNumber of genes that overlapped relative to the number expected by chance.^fThe core of the binding sequence of class I and II TCP domains (Kosugi and Ohashi 2002)^gThe binding sequence of the class II TCP domain (Kosugi and Ohashi 2002)Reference: Kosugi S, Ohashi Y. 2002. DNA binding and dimerization specificity and potential targets for the TCP protein family. *Plant J* **30**: 337-348.

Supplemental Table 3. Changes of the expression of 24 out of 78 genes encoding auxin-inducible proteins upon expression of *TCP3SRDX* determined by microarray analysis of *ProXVE:TCP3SRDX* and *ProXVE:TCP3SRDX cuc1* plants.

AGI code	<i>ProXVE:TCP3SRDX</i>					<i>ProXVE:TCP3SRDX cuc1</i>						
	^a Change	^a P value	^a Signal values (Estr/DMSO)			^a Change	^a P value	^a Signal values (Estr/DMSO)			^b GnCCC	
AT1G29450	0.024	0.0024	0.017/0.499	0.009/0.458	0.008/0.474	0.100	0.0045	0.029/0.182	0.019/0.213	0.035/0.320	0.010/0.290	+
AT1G29440	0.032	0.0005	0.027/0.820	0.021/0.803	0.026/0.760	0.100	0.0016	0.057/0.395	0.039/0.454	0.069/0.604	0.031/0.591	+
AT1G29460	0.031	0.0065	0.011/0.253	0.007/0.249	0.004/0.274	0.143	0.0216	0.022/0.080	0.013/0.103	0.022/0.165	0.003/0.124	+
AT4G38850	0.055	0.0292	0.005/0.227	0.004/0.220	0.028/0.237	0.084	0.0039	0.001/0.027	0.001/0.060	0.007/0.046	0.002/0.036	+
AT4G38840	0.054	0.0010	0.189/2.974	0.146/2.734	0.130/2.838	0.109	0.0005	0.249/2.175	0.259/2.336	0.354/2.491	0.201/2.813	+
AT3G03850	0.059	0.0045	0.008/0.195	0.008/0.149	0.010/0.126	0.164	0.0006	0.022/0.166	0.040/0.182	0.038/0.221	0.024/0.190	+
AT5G18050	0.070	0.0003	0.061/0.954	0.063/0.831	0.057/0.818	0.210	0.0030	0.186/0.650	0.137/0.699	0.217/0.918	0.084/0.683	-
AT5G18020	0.077	0.0010	0.035/0.396	0.027/0.395	0.024/0.349	0.195	0.00605	0.051/0.167	0.034/0.186	0.055/0.298	0.019/0.201	+
AT2G37030	0.083	0.0142	0.009/0.228	0.011/0.133	0.017/0.148	0.391	0.0175	0.011/0.020	0.009/0.043	0.014/0.038	0.011/0.026	+
AT5G18010	0.035	0.0048	0.016/0.321	0.008/0.284	0.006/0.257	0.137	0.0012	0.033/0.178	0.025/0.186	0.042/0.294	0.015/0.183	+
AT5G18030	0.054	0.0011	0.031/0.480	0.020/0.433	0.019/0.391	0.188	0.0069	0.072/0.216	0.036/0.257	0.070/0.380	0.023/0.251	+
AT5G18080	0.087	0.0065	0.033/0.356	0.026/0.314	0.023/0.287	0.271	0.0155	0.077/0.164	0.043/0.189	0.066/0.272	0.026/0.194	+
AT4G38860	0.088	0.0024	0.097/0.919	0.086/1.238	0.097/1.082	0.122	0.0018	0.090/0.661	0.079/0.636	0.095/0.585	0.043/0.679	+
AT5G18060	0.114	0.0001	0.063/0.568	0.057/0.511	0.055/0.458	0.285	0.0055	0.147/0.353	0.104/0.394	0.159/0.555	0.074/0.432	-
AT3G03820	0.127	0.0010	0.031/0.282	0.029/0.211	0.027/0.211	0.196	0.0007	0.049/0.271	0.050/0.287	0.092/0.340	0.047/0.294	-
AT1G29430	0.093	0.0054	0.006/0.053	0.004/0.059	0.003/0.054	0.138	0.0005	0.001/0.021	0.002/0.015	0.002/0.015	0.003/0.021	+
AT2G21210	0.068	0.0057	0.103/1.060	0.084/1.419	0.078/1.592	0.106	0.0028	0.084/0.829	0.074/0.894	0.131/0.695	0.064/1.181	-
AT2G18010	0.196	0.0013	0.020/0.115	0.021/0.112	0.020/0.091	0.623	0.0238	0.039/0.054	0.029/0.064	0.038/0.067	0.058/0.079	-
AT1G29510	0.185	0.0002	0.108/0.618	0.112/0.589	0.112/0.589	0.309	0.0005	0.135/0.358	0.120/0.443	0.182/0.586	0.150/0.540	+

AT1G29420	0.149	0.0068	0.003/0.029	0.003/0.017	0.002/0.019	0.301	0.0157	0.004/0.010	0.002/0.018	0.004/0.024	0.003/0.008	+
AT4G34760	0.084	0.0000	0.186/2.236	0.228/2.745	0.202/2.340	0.183	0.0001	0.266/1.547	0.323/1.651	0.340/1.587	0.275/1.811	+
AT1G72430	0.252	0.0033	3.375/12.13	3.307/15.46	4.352/16.43	0.304	0.0348	1.912/6.130	1.462/7.669	5.010/8.178	1.174/11.59	-
AT1G29500	0.333	0.0104	0.158/0.603	0.184/0.486	0.191/0.533	0.419	0.0130	0.204/0.307	0.117/0.371	0.176/0.475	0.141/0.434	+
AT1G75590	0.381	0.0412	0.027/0.104	0.031/0.092	0.045/0.084	0.464	0.0113	0.030/0.069	0.030/0.096	0.038/0.084	0.059/0.092	-
AT4G09530	0.421	0.0430	0.003/0.011	0.002/0.007	0.002/0.004	0.214	0.0035	0.001/0.010	0.002/0.006	0.002/0.016	0.003/0.014	-

^aChanges were average ratios of the signal values of the plants exposed to DMSO relative to those from plants exposed to 5 µM estradiol (Estr) for 24 h in liquid medium. The average values were obtained from three (*ProXVE:TCP3SRDX*) and four (*ProXVE:TCP3SRDX cuc1*) replicates. Signal values were calculated by dividing raw values by median values of all filter-passed spots (see Methods). P values were obtained as described in Methods.

^bGGnCCC motif was present (+) or absent (-) in the 1,000-bp upstream region of each respective gene (<http://www.arabidopsis.org/>).

Supplemental Table 4. Changes of expression of genes for the IAA/AUX family from the microarray analysis of *ProXVE:TCP3SRDX* and *ProXVE:TCP3SRDX cuc1* plants.

AGI code	Name	<i>ProXVE:TCP3SRDX</i>						<i>ProXVE:TCP3SRDX cuc1</i>						^b GGnCCC
		^a Change	^a P value	^a Signal values (Estr/DMSO)			^a Change	^a P value	^a Signal values (Estr/DMSO)					
AT1G04240	IAA3	0.108	0.0039	0.125/1.347	0.137/1.504	0.207/1.472	0.140	0.0009	0.171/1.121	0.196/1.210	0.232/1.454	0.112/1.310	-	-
AT3G15540	IAA19	0.184	0.0026	0.079/0.499	0.099/0.562	0.103/0.479	0.246	0.0002	0.051/0.222	0.059/0.220	0.078/0.283	0.067/0.324	-	-
AT4G28640	IAA11	0.294	0.0017	0.282/1.046	0.335/1.158	0.339/1.052	0.362	0.0013	0.289/0.798	0.289/0.814	0.325/0.732	0.280/0.967	+	+
AT5G43700	IAA4	0.308	0.0038	1.809/6.831	2.376/7.165	2.357/7.162	0.435	0.0014	2.291/5.050	2.284/5.551	2.559/4.998	2.271/6.262	-	-
AT1G04250	IAA17	0.455	0.0087	2.818/6.574	3.522/8.518	4.372/8.325	0.394	0.0000	3.672/9.850	3.750/9.953	4.204/10.24	4.896/11.69	-	-
AT4G29080	IAA27	0.382	0.0059	0.501/1.526	0.675/1.702	0.711/1.685	0.407	0.0012	0.540/1.429	0.584/1.602	0.771/1.526	0.624/1.634	+	+

For (a) and (b), see footnote to Supplemental Table 3.

Supplemental Table 5. Changes of expression of genes for the PIN family from the microarray analysis of *ProXVE:TCP3SRDX* and *ProXVE:TCP3SRDX cuc1* plants.

AGI code	Name	<i>ProXVE:TCP3SRDX</i>					<i>ProXVE:TCP3SRDX cuc1</i>					^b GGnCCC	
		^a Change	^a P value	^a Signal values (Estr/DMSO)			^a Change	^a P value	^a Signal values (Estr/DMSO)				
AT1G73590	<i>PIN1</i>	3.361	0.0084	1.827/0.441	2.453/0.836	2.244/0.746	1.744	0.0072	1.446/0.870	1.275/0.895	1.534/0.871	2.174/1.019	-
AT5G57090	<i>PIN2</i>	1.041	0.2500	0.217/0.201	0.370/0.352	0.335/0.338	1.120	0.2817	0.468/0.467	0.501/0.467	0.475/0.473	0.743/0.530	-
AT1G70940	<i>PIN3</i>	0.087	0.0009	0.128/1.469	0.141/1.857	0.145/1.462	0.135	0.0001	0.164/1.441	0.241/1.698	0.250/1.526	0.206/1.679	-
AT2G01420	<i>PIN4</i>	0.096	0.0000	0.267/2.866	0.380/0.4020	0.342/3.408	0.195	0.0017	0.320/1.972	0.365/2.356	0.523/1.749	0.331/1.988	-
AT5G16530	<i>PIN5</i>	3.055	0.0674	0.205/0.078	0.363/0.076	0.311/0.173	3.902	0.0034	0.108/0.024	0.082/0.032	0.149/0.028	0.220/0.062	-
AT1G77110	<i>PIN6</i>	3.640	0.0010	0.200/0.057	0.294/0.084	0.279/0.070	2.123	0.0000	0.314/0.137	0.262/0.126	0.263/0.124	0.332/0.165	-
AT1G23080	<i>PIN7</i>	0.091	0.0012	0.190/1.998	0.176/2.281	0.209/2.031	0.137	0.0005	0.267/2.640	0.335/2.585	0.463/2.456	0.411/3.128	-

For (a) and (b), see footnote to Supplemental Table 3.

Supplemental Table 6. Changes in expression of the genes for organ morphogenesis determined by microarray analysis of *ProXVE:TCP3SRDX* and *ProXVE:TCP3SRDX cuc1* plants.

AGI code	Name	<i>ProXVE:TCP3SRDX</i>					<i>ProXVE:TCP3SRDX cuc1</i>					^b GGnCCC	
		^a Change	^a P value	^a Signal values (Estr/DMSO)			^a Change	^a P value	^a Signal values (Estr/DMSO)				
AT2G37630	AS1	0.264	0.0018	0.773/3.286	1.051/3.855	0.904/3.171	0.433	0.0051	2.178/6.903	2.696/6.502	2.294/5.114	2.906/5.247	+
AT4G01500	NGA4	0.329	0.0098	0.016/0.060	0.022/0.071	0.016/0.042	0.273	0.0008	0.028/0.118	0.030/0.132	0.030/0.113	0.038/0.109	+
AT1G01030	NGA3	0.338	0.0000	0.101/0.302	0.122/0.355	0.116/0.349	0.353	0.0013	0.113/0.411	0.149/0.364	0.139/0.353	0.143/0.430	-
AT1G14920	GAI	0.189	0.0027	0.667/2.985	0.777/4.483	0.560/3.283	0.266	0.0001	1.022/4.206	0.968/3.791	1.054/3.472	1.052/3.966	-
AT5G41410	BEL1	0.412	0.0073	0.516/1.081	0.566/1.484	0.488/1.294	0.339	0.0004	0.336/1.218	0.437/1.204	0.360/0.996	0.495/1.397	-
AT5G03680	PTL	0.407	0.0026	0.065/0.164	0.069/0.183	0.079/0.180	0.407	0.0028	0.098/0.285	0.139/0.292	0.147/0.307	0.125/0.381	+
AT2G26580	YAB5	0.222	0.0017	0.215/1.093	0.233/0.949	0.223/0.988	0.323	0.0029	0.351/1.044	0.344/0.978	0.444/1.143	0.345/1.594	+
AT4G36870	SAW1	0.444	0.0162	0.316/0.583	0.409/1.065	0.323/0.793	0.399	0.0010	0.202/0.610	0.229/0.608	0.210/0.472	0.271/0.612	-
AT3G17185	TAS3	0.449	0.0114	0.138/0.281	0.130/0.347	0.175/0.363	0.248	0.0009	0.033/0.121	0.039/0.161	0.055/0.186	0.039/0.220	+
AT1G69440	AGO7	0.311	0.0176	0.230/0.552	0.230/0.908	0.216/0.825	0.299	0.0002	0.359/1.330	0.389/1.204	0.417/1.239	0.426/1.599	+
AT5G67440	NPY3	0.435	0.0035	0.988/2.251	1.334/3.359	1.122/2.382	0.449	0.0000	1.175/2.456	1.328/2.953	1.131/2.664	1.274/2.861	+

For (a) and (b), see footnote to Supplemental Table 3.

Supplemental Table 7. Changes in expression of genes that control developmental timing upon expression of *TCP3SRDX*

AGI code	Name	<i>ProXVE:TCP3SRDX</i>						<i>ProXVE:TCP3SRDX cuc1</i>						^b GGnCCC	Reference
		^a Change	^a P value	^a Signal values (Estr/DMSO)			^a Change	^a P value	^a Signal values (Estr/DMSO)						
AT2G39250	SNZ	0.275	0.0008	0.268/0.918	0.318/1.244	0.314/1.134	0.386	0.0018	0.435/0.985	0.469/1.037	0.449/1.393	0.451/1.376	+	Schmid et al. 2003	
AT1G25560	TEM1	0.494	0.0144	8.537/19.78	11.23/23.76	11.61/20.06	0.453	0.0002	7.197/16.48	8.117/16.16	6.526/14.33	6.980/16.54	-	Castillejo et al. 2008	
AT1G68840	TEM2	0.453	0.0233	5.155/14.80	7.593/15.12	7.643/14.94	0.386	0.0003	5.248/12.95	4.968/12.00	4.495/11.30	4.733/14.44	-	Castillejo et al. 2008	
AT2G41940	ZFP8	0.102	0.0006	0.171/1.494	0.151/1.600	0.161/1.660	0.170	0.0005	0.282/1.634	0.271/1.535	0.337/1.615	0.213/1.738	-	Gan et al. 2006	
AT3G58070	GIS	0.113	0.0008	0.087/0.717	0.083/0.715	0.075/0.755	0.228	0.0004	0.227/1.039	0.227/1.013	0.264/0.927	0.190/1.030	-	Gan et al. 2006	
AT1G25250	IDD16	0.296	0.0022	0.088/0.274	0.100/0.378	0.092/0.307	0.289	0.0004	0.124/0.367	0.122/0.399	0.121/0.444	0.131/0.548	-	Colasanti et al. 1998	
AT2G02080	IDD4	0.204	0.0019	0.794/3.413	0.763/3.908	0.641/3.476	0.305	0.0024	0.952/3.123	1.060/3.124	1.137/3.069	0.735/3.534	+	Colasanti et al. 1998	
AT4G14540	NF-YB3	0.242	0.0004	2.572/11.07	3.038/11.80	2.824/11.80	0.329	0.0031	4.598/11.79	4.817/13.94	4.977/13.72	3.447/15.63	+	Kumimoto et al. 2008	
AT5G15840	CO	0.202	0.0081	0.015/0.102	0.027/0.126	0.027/0.115	0.245	0.0035	0.027/0.113	0.025/0.120	0.037/0.101	0.020/0.125	+	Putterill et al. 1995	
AT2G33810	SPL3	0.291	0.0031	0.100/0.396	0.124/0.418	0.122/0.377	0.381	0.0085	0.056/0.106	0.057/0.147	0.053/0.149	0.040/0.164	+	Cardon et al. 1997	
AT1G14920	GAI	0.189	0.0027	0.667/2.985	0.777/4.483	0.560/3.283	0.266	0.0001	1.022/4.206	0.968/3.791	1.054/3.472	1.052/3.966	-	Gan et al. 2006	
AT1G66350	RGL1	0.401	0.0044	0.368/0.814	0.376/0.994	0.351/0.939	0.351	0.0013	0.504/1.873	0.617/1.661	0.647/1.829	0.842/2.048	-	Wen and Chang 2002	

For (a) and (b), see footnote to Supplemental Table 3.

References

- Cardon G, Höhmann S, Nettesheim K, Saedler H, Huijser P. 1997. Functional analysis of the *Arabidopsis thaliana* SBP-box gene SPL3: a novel gene involved in the floral transition. *Plant J* **12**: 367-377.
- Castillejo C, Pelaz S. 2008. The balance between CONSTANS and TEMPRANILLO activities determines FT expression to trigger flowering. *Curr Biol* **18**: 1338-1343.
- Colasanti J, Yuan Z, Sundaresan V. 1998. The indeterminate gene encodes a zinc finger protein and regulates a leaf-generated signal required for the transition to flowering in maize. *Cell* **93**: 593-603.
- Gan Y, Kumimoto R, Liu C, Ratcliffe O, Yu H, Broun P. 2006. GLABROUS INFLORESCENCE STEMS modulates the regulation by gibberellins of epidermal differentiation and shoot maturation in *Arabidopsis*. *Plant Cell* **18**: 1383-1395.

- Kumimoto RW, Adam L, Hymus GJ, Repetti PP, Reuber TL, Marion CM, Hempel FD, Ratcliffe OJ. 2008. The Nuclear Factor Y subunits NF-YB2 and NF-YB3 play additive roles in the promotion of flowering by inductive long-day photoperiods in *Arabidopsis*. *Planta* **228**: 709–723.
- Putterill J, Robson F, Lee K, Simon R, Coupland G. 1995. The CONSTANS gene of *Arabidopsis* promotes flowering and encodes a protein showing similarities to zinc finger transcription factors. *Cell* **80**: 847-857.
- Schmid M, Uhlenhaut N, Godard F, Demar M, Bressan R, Weigel D, Lohmann J. 2003. Dissection of floral induction pathways using global expression analysis. *Development* **130**: 6001-6012.
- Wen C, Chang C. (2002) *Arabidopsis RGL1* Encodes a Negative Regulator of Gibberellin Responses. *Plant Cell* **14** 87-100.

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Primers used in this study

The regions with red letters were the sites of restriction enzymes used for construction of plasmids.

name	sequence	purpose
AT1G53230F	ATGGCACCAGATAACGACCATTTC	For amplifying TCP3 gene in RT-PCR analysis
AT1G53230R	ATGGCGAGAATCGGATGAAGC	For amplifying TCP3 gen in RT-PCR analysis
AT2G31070F	ATGGGACTTAAAGGATATAGCG	For amplifying TCP10 gene in RT-PCR analysis
AT2G31070R	GAGGTGTGAGTTGGAGGAG	For amplifying TCP10 gene in RT-PCR analysis
AT3G15030F	ATGTCTGACGACCAATTCCATC	For amplifying TCP4 gen in RT-PCR analysis
AT3G15030R	ATGGCGAGAAATAGAGGAAGCAG	For amplifying TCP4 gene in RT-PCR analysis
AT3G15030S	TCAATGGCGAGAAATAGAGGAAGCAG	For amplifying TCP4 gene in RT-PCR analysis
AT1G30210F	ATGGAGGTTGACGAAGACATTG	For amplifying TCP24 gene in RT-PCR analysis
AT1G30210R	TCTCCTTCCCTTGCCCTTGTC	For amplifying TCP24 gene in RT-PCR analysis
AT4G18390F	ATGATTGGAGATCTAATGAAG	For amplifying TCP2 gene in RT-PCR analysis
AT4G18390R	GTTCTTGCCTTACCCCTTATG	For amplifying TCP2 gene in RT-PCR analysis
AT4G18390S	TCAGTTCTGCCTTACCCCTTATG	For amplifying TCP2 gene in RT-PCR analysis
AT5G08070F	ATGGGAATAAAAAAGAAGATCAG	For amplifying TCP17 gene in RT-PCR analysis
AT5G08070R	CTCGATATGGCTGGTTGTGAG	For amplifying TCP17 gene in RT-PCR analysis
AT5G60970F	ATGAGATCAGGAGAACATGTGATG	For amplifying TCP5 gene in RT-PCR analysis
AT5G60970R	AGAATCTGATTCAATTATCGCTAC	For amplifying TCP5 gene in RT-PCR analysis
AT3G02150F	ATGAATATCGTCTTGGAAAGATG	For amplifying TCP13 gene in RT-PCR analysis
AT3G02150R	CATATGGTGTACTTCCTCTACTTG	For amplifying TCP13 gene in RT-PCR analysis
#745	ATGAAAGAGAGACAACGTTGGAGTG	For amplifying AS1 gene in RT-PCR analysis
#746	CGGCATCATACTCCCTAACACAAG	For amplifying AS1 gene in RT-PCR analysis
#4741	CATTCAACCACTTCATTACTTCAGAG	For amplifying Atlg29460 gene in RT-PCR analysis
#4751	CAGAGGAAAAAAATGTCTACACTC	For amplifying Atlg29460 gene in RT-PCR analysis
#4735	CATCAACAAACAACAGCAATCC	For amplifying At5g18020 gene in RT-PCR analysis
#4736	GCATAAAAGATGGCATTTACTCTC	For amplifying At5g18020 gene in RT-PCR analysis
H0411	GATGGATGAGTTGTTAACCTCAAGGAAAC	For amplifying IAA3 gene in RT-PCR analysis
H0412	TACACCACAGCCTAACACCTTGCGCTCTGA	For amplifying IAA3 gene in RT-PCR analysis
H2245	GATGGAAAAAGTTGATGTTATGATGAGCT	For amplifying IAA4 gene in RT-PCR analysis
H2246	AAGACCACCACAACCTAACCTTAACCTC	For amplifying IAA4 gene in RT-PCR analysis
H1508	GATGGCATCTTCCGGTAACGGTACAACGGC	For amplifying LBD16 gene in RT-PCR analysis
H1509	GTTCTTCATCATTCTAACAGAGCAAAGCCTG	For amplifying LBD16 gene in RT-PCR analysis
#629	GCGGCGTAGTTAGTAGAGAGACGAAC	For amplifying CUC1 gene in RT-PCR analysis
#1720	AGGAAGAACCGTGGGAGGCAGAGAAGGTAG	For amplifying CUC1 gene in RT-PCR analysis

TK0014	GAGTAATTGGTTATGCATGAATATCG	For amplifying CUC2 gene in RT-PCR analysis
TK0015	GTAGTTCCAAATACAGTCAGTCC	For amplifying CUC2 gene in RT-PCR analysis
#2325	CGACCATTACACCGGCCACACG	For amplifying CUC3 gene in RT-PCR analysis
#1529	CAGCTGGAATCCTAAAGGACATGGAGAAC	For amplifying CUC3 gene in RT-PCR analysis
#2333	ATGGCGTCGTCATCAAACATCAC	For amplifying LOB gene in RT-PCR analysis
#2334	TCACATGTTACCTCCTGCTGATC	For amplifying LOB gene in RT-PCR analysis
#1910	TGTTGGTTAAATATCGTGAGGAGC	For amplifying KNAT1 gene in RT-PCR analysis
#1912	TCATGGACCGAGACGATAAGGTCC	For amplifying KNAT1 gene in RT-PCR analysis
#1558	TGTCAGATCCGGTCCCGTACGGTCAG	For amplifying TUB gene in RT-PCR analysis
#1559	CACTCATGGTTGCAGAGATGAGGTG	For amplifying TUB gene in RT-PCR analysis
#5201	AATAAA GTGAC AGCTAGGGAGTAAAGGTCC	For insertion of the At1g29460 promoter in pBI101
#5071	ATTAAA GGATCC TTTACTAATAGAAAGAGAGCAAACAAAAAGGG	For insertion of the At1g29460 promoter in pBI101
#5072	GCAGATATGATTGATTACTAGTTGGAAACTCTTAGACAAGAACTAC	For site-directed mutagenesis of the At1g29460 promoter
#5073	GTAGTTCTGTCTAAAGAGTTCCAAACTAGTAATCAATCATATCTGC	For site-directed mutagenesis of the At1g29460 promoter
#5074	CATCTCTGAGAACATGAGAGAACCGCATTTTCTTCACC	For site-directed mutagenesis of the At1g29460 promoter
#5075	GGTGAAGAAAAGATGCGGTTCTCATGTTCTCAGAGATG	For site-directed mutagenesis of the At1g29460 promoter
#5076	GGGTTTCGGTTCAAGCTTCTCG	For ChIP analysis of the At1g29460 promoter
#5077	GAAGAATGCTCTAACGCTTGTGC	For ChIP analysis of the At1g29460 promoter
#5897	CTTGTGAGATGGTGTCTCTG	For ChIP analysis of the control of At1g29460 gene
#5898	CCTCAAGTGGAACATTCCCTGC	For ChIP analysis of the control of At1g29460 gene
TK0009	CACTCTAATTTCGTTGGTTAACATGC	For ChIP analysis of the IAA3 promoter
TK0010	GTTCGTAATTGTATTGCGACATG	For ChIP analysis of the IAA3 promoter
TK0012	ACCCATTTCATTTGGTCACTAG	For ChIP analysis of the control of IAA3 gene
TK0013	TCATTACTACGGCCTGTCTAGTC	For ChIP analysis of the control of IAA3 gene
#5424	GGTAGTCGGATGTGATGGAAC	For ChIP analysis of the AS1 promoter
#5425	GCAATGAGAACAGAGATAAACATCAC	For ChIP analysis of the AS1 promoter
#5891	ATGAGCTGGTTTGCGCTGTC	For ChIP analysis of the control of AS1 gene
#5896	CTTTGTACATTTTGCAGAGCAAACG	For ChIP analysis of the control of AS1 gene
#5355	CTAGAGATCATATTACCTATCCTGAG	For ChIP analysis of the miR164A promoter
#5356	GTATATCATGATAAAATGCCGAAGC	For ChIP analysis of the miR164A promoter
#5892	GTTTGAGTTCTCATCTTGCTTAGC	For ChIP analysis of the control of miR164A gene
#5893	TAGTCTAGTCAACGCCCTGTCTC	For ChIP analysis of the control of miR164A gene
#5438	GTTATGGGAGAGAGAACATTATTACACACTACATGC	For site-directed mutagenesis of the AS1 promoter
#5439	GCATGTAAGTGTGATAATAATGTTCCCTCTCTCCATAAC	For site-directed mutagenesis of the AS1 promoter
#5481	ATAAA AGATCT CCTGAGTCCATGTGTGGACTG	For insertion of the miR164A promoter in the LUC reporter
#5480	ATTAAA GTGAC GGAGATTCTCACCGCATT	For insertion of the miR164A promoter in the LUC reporter
#5494	GAGGAATGGTATCAACATAGGAAACTTTTTCCATGTTAGAG	For site-directed mutagenesis of the miR164A promoter

#5495	CTCTAACATGGAAAAAAAAAGTTCTATGTTGATACCATTCC	For site-directed mutagenesis of the miR164A promoter
#35	GAAGTTCATTCATTGGAGAGG	For cloning of AS1, miR164A, IAA3, At1g29460 genes
#1949	ACGC GTCGAC TCAGGGCGGTCTAATCTGCAAC	For cloning of AS1 gene
#5768	AATAAA GTCGAC GAAACGAATAACGGTCCATGC	For cloning of miR164A gene
#4569	ATTAAA GTCGAC TCATACACCCACAGCCTAAACC	For cloning of IAA3 gene
#4914	ATTAAA GTCGAC TAAAATACAAGTAATTGTTGGGTATAACCAC	For cloning of At1g29460 gene
#2297	CATCATCATCATCATCAGCAGTCC	For cloning of TCP3C (TCP3 CDS contains the Eco RI site.)
TK0037	ATAAA GAATT TCGGGTTTCGCATACCAG	For cloning of TCP4C
TK0038	ATAAA GAATT CATGATGCAAGGCCTTAGTTCC	For cloning of TCP10C
Tnos-RV	CCCATCTCATATAAACGTC	For cloning of TCP3C, TCP4C, and TCP10C